

Amendments to the Drawings:

The attached 12 sheets of drawings include changes to Figs. 2, 6A-7:

Replacement Sheets 2/19-3/19 (Fig. 2), replace originally submitted sheets 2/19-3/19 (Fig. 2).

Replacement Sheets 7/19-13/19 (Figs 6A-6D), replace originally submitted sheets 7/19-13/19 (Figs. 6A-6D).

Replacement Sheets 14/19-16/19 (Fig. 7), replace originally submitted sheets 14/19-16/19 (Fig. 7).

The Amendments to the Drawings are made to incorporate the sequence identifier numbers. Applicant has submitted a "Marked-up" version of original sheets 2/19-3/19 and 7/19-16/19.

Attachment: 24 sheets of drawings, i.e., 12 "Replacement" and 12 "Marked-Up" sheets of drawings.

REMARKS


Applicants submit that the substitute specification and replacement drawings are filed simply to incorporate the sequence identifier numbers. No new matter is added.

Applicant submits that all claims are allowable as written and respectfully request early favorable action by the Examiner. If the Examiner believes that a telephone conversation with Applicant's attorney/agent would expedite prosecution of this application, the Examiner is cordially invited to call the undersigned attorney/agent of record.

Date:

3-30-2005

Respectfully submitted,



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MARKED-UP VERSION

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FIGURE 2

Score = 553 bits (1425), Expect = e-156
Identities = 327/700 (46%), Positives = 406/700 (57%), Gaps = 152/700 (21%)

Query: 1
Sbjct: 1
Beta-strand region 50
Hydrogen bonded turn 48
Beta-strand region 41
Hydrogen bonded turn 38
Beta-strand region 28
Hydrogen bonded turn 26
Helical region 13
Beta-strand region 7
SH2 1. 6
Hydrogen bonded turn 5
PTPN11 1

MSSRRWFHPTISGIEAEKLLQEQQGFDGSLARLSSSNPGAFTLVRRGNEVTHIKIQNNG 60
M+SRWFHP I+G+EAE LL +G DGSFLAR S SNPG FTLSVRR VTHIKIQN G
MTSRRWFHPNITGVEAENLLLTRGVDGSLARPSKSNPGDFTLSVRRNGAVTHIKIQNTG 60

(SEQ ID NO:279)

(SEQ ID NO:280)

Query: 61
Sbjct: 61
Hydrogen bonded turn 83
Helical region 74
Beta-strand region 70
Hydrogen bonded turn 66
Beta-strand region 63
SH2 1. 61
PTPN11 61
Hydrogen bonded turn 85
Helical region 119
Beta-strand region 113
SH2 2. 112
Hydrogen bonded turn 111
Hydrogen bonded turn 108
Beta-strand region 100
Beta-strand region 95
Beta-strand region 89

61 DFFDLYGGEKFATLPELVQYYMEN-GELKEKNGQAIELKQPLICAEPPTERWFHGNLSGK 119
D++DLYGGEKFATL ELVQYYME+ G+LKEKNG IELK PL CA+PT+ERWPHG+LSGK
DYDDLYGGEKFATLAEVLQYYMEHGLKEKNGDVIELKYPLNCADPTSERWFHGHLSGK 120

Query: 120
Sbjct: 121
Beta-strand region 147
Hydrogen bonded turn 144
Beta-strand region 134
Hydrogen bonded turn 132
Hydrogen bonded turn 129
Helical region 121
SH2 2. 121
PTPN11 121
Beta-strand region 178
Hydrogen bonded turn 176
Beta-strand region 166

120 EAEKLILERGKNGSFLVRESQSKPGDFVLSVRTD-----KVTHVMIRWQDKKYD 169
EAEKL+ E+GK+GSFLVRESQS PGDFVLSVRT D KVTHVMIR Q+ KYD
121 EAEKLITEKGKHSFLVRESQSHPGDFVLSVRTGDDKKGESNDGKSKVTHVMIRQCELKYD 180

Query: 170
Sbjct: 181
Helical region 223
Beta-strand region 221
Beta-strand region 214
Beta-strand region 209
Hydrogen bonded turn 205
Beta-strand region 203
Helical region 190
Beta-strand region 187
PTPN11 181
SH2 2. 181
Helical region 226

170 VGGGESFGTLSELIDHYKRNPMVETCGTVVHLRQPFNATRITAAGINARVEQLVKGGFWE 229
VGGGE F +L++L++HYK+NPMVET GTV+ L+QP N TRI A A +E V+
181 VGGGERFDSLTDLVEHYKKNPMVETLGTVLQLKQPLNTRINA----AEIESRVR----- 231

Query: 230
Sbjct: 232
Helical region 266
Helical region 256
Helical region 247
PTPN11 232
Helical region 232

230 EFESLQQDSRDTSPSRNEGYKQENRLKNRYRNILPYDHTRVKLLDVEHSVAGAEYINANYI 289
L + + T +G+ +E + L Y
232 ---ELSKLAETTDKVKQGFWEFETLQQQCECKLLYSRKE----- 267

Query: 290
RLPTDGDLYNMSSSSSESLNSSVPSPACTAAQTQRNCSNCQLQNKTCVQCAVKSAILPYS 349
Q Q N + + +N ILP+

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Sbjct:                268 -----GQRQENKKNRYKN-----ILPPD 286
Hydrogen bonded turn  280
PROTEIN-TYROSINE PHOSPHATASE. 276
                                *****
Helical region        271
                                *****
PTPN11                268
                                ++++++
Helical region        268
                                **
Hydrogen bonded turn  286
                                .

Query:                350 NCATCSRKSDSLSKHKRSESSASSPSSSGSGPGSSGTSVSSVNGPGTPTNLTSGTAG 409
                                +      D                      P P +
Sbjct:                287 HTRVVLHDGD-----PNEPVS----- 302
Beta-strand region    289 ***
Hydrogen bonded turn  287 **
PTPN11                287 ++++++
PROTEIN-TYROSINE PHOSPHATASE. 287 *****

Query:                410 CLVGLLKRHSNDSSGAVSISMAERERE-REREMFKTYIATQGCLLTQQVNTVTDVFNVMVW 468
                                D A + I M E E + + K+YIATQGCL NTV DFW MV+
Sbjct:                303 -----DYINA-NIIMPEFETKCNNSKPKSYIATQGCLQ-----NTVDFWRMVV 346
Beta-strand region    304
                                *****
PTPN11                303
                                ++++++
PROTEIN-TYROSINE PHOSPHATASE. 303
                                *****
Hydrogen bonded turn  335
                                *
Beta-strand region    327
                                ****
Helical region        338
                                *****

Query:                469 QENTRVIVMTTKEYERGKEKCARYWPDGRSEQFGHARIQCVSENSTSDYTLREFLVSWR 528
                                QEN+RVIVMTTKE ERGK KC +YWPDE +++G R++ V E++ DYTLRE +S
Sbjct:                347 QENSRVIVMTTKEYERGKSKCVKYWPDEYALKEYGVMRVNRVKESAAHDYTLRELKLSKV 406
Hydrogen bonded turn  406
Beta-strand region    396
Beta-strand region    383
Hydrogen bonded turn  381
Beta-strand region    377
Hydrogen bonded turn  374
Beta-strand region    364
Hydrogen bonded turn  362
Beta-strand region    360
Beta-strand region    352
Hydrogen bonded turn  349
Helical region        347
PTPN11                347 ++++++
PROTEIN-TYROSINE PHOSPHATASE. 347 *****

Query:                529 DQ--PARRIFHYHFQVWPDHGVDPADPGCVLNFQLQDVNTRQSHLAQAGEKPGPICVHCSAG 586
                                Q R ++ YHF+ WPDHGV+DPG VL+FL++V+ +Q + AG P+ VHCSAG
Sbjct:                407 GQGNTERTVWQYHFRTPDGHVPSDPGGVLDLFEEVHHKQESIMDAG---PVVVHCSAG 462
Beta-strand region    408
Hydrogen bonded turn  407 *
PTPN11                407 ++++++
PROTEIN-TYROSINE PHOSPHATASE. 407
Hydrogen bonded turn  450
Helical region        432
active                459
Beta-strand region    455

Query:                587 IGRGTGTFIVDMILDQIVRNGLDTEIDIQRTIQMVRSQRSGLVQTEAQYKFVYVAVQHYI 646
                                IGRGTGTFIVD+++D I G+D +ID+ +TIQMVRSGRSG+VQTEAQY+F+Y AVQHYI
Sbjct:                463 IGRGTGTFIVDILIDIIREKGVDCDIDVPKTIQMVRSGRSGMVQTEAQYRFIYMAVQHYI 522
Helical region        508
Hydrogen bonded turn  502
Hydrogen bonded turn  499
Helical region        490
Beta-strand region    487
Hydrogen bonded turn  484
Helical region        464
PTPN11                463 ++++++
PROTEIN-TYROSINE PHOSPHATASE. 463 *****

Query:                647 QTLIARKRAEEQSLQVGREYTNIKYTGEIGNDSQRSPLPP 686
                                +TL R E++S + G EYTNIKY+ +SPLPP
Sbjct:                523 ETLQRRIEEEQSKRKGEYTNIKYSLADQTSQDQSPPLP 562
Conflict              548
phosphorylation       542
Conflict              535
Hydrogen bonded turn  524
Helical region        523
PTPN11                523 ++++++

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FIGURE 6A

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 1

BLAST P sequence alignment

Score = 616 bits (1588), Expect = e-175
Identities = 306/517 (59%), Positives = 390/517 (75%), Gaps = 24/517 (4%)

Query: 453 QPGSRYASTNVLAAPPPTPRAVST-----EDITREPTITIQKGPQGLGFNIVGGE 504
QP + S + P + P S ++ITREPR + + +G GLGFNIVGGE
Sbjct: 425 QPVDNHVSPSSFLGQTPASPARYSPVSKAVLGDDDEITREPRKVVLRHGSTGLGFNIVGGE 484

Query: 505 DGQGIYVSFILAGGPADLGSSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTLAQ 564
DG+GI++SFILAGGPADL EL++GD+++SVN+V+L A+HE+AA ALK +G VT++AQ
Sbjct: 485 DGEFIFISFILAGGPADLGSSELKRGDRIISVNSVDLRAASHEQAAAAALKNAGQAVTIVAQ 544

Query: 565 YRPEEYNRFEARIQELKQXXXXXXXXXXXX-XXQKRSLYVRALFDYDPNRDDGLPSRG 623
YRPEEY+RFEA+I +L++Q QKRSLYVRALFDYD +D GLPS+G
Sbjct: 545 YRPEEYSRFEAKIHDLREQMNSSISSGSGSLRTSQKRSLYVRALFDYDKTKDSGLPSQG 604

Query: 624 LPFKHGDILHVTNASDDEWQARRVLGDNEDEQIGIVPSKRRWERKMRARDRSVKFQGHA 683
L FK GDILHV NASDDEWQAR+V D E +++G++PSKRR E+K RAR ++VKF
Sbjct: 605 LNFKPGDILHVINASDDEWQARQVTPDGESDEVGVIPSKRRVEKKERARLKTVKFN--- 661

Query: 684 AANNLNDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEGDSDQEPNGVVSSTSEIDIXXXX 743
+ DK + + K+K FSRKFPF K++D+ ++ SD + + V S+ S+ +
Sbjct: 662 --SKTRDKQSFNDKRKKNLFSRKFPFYKNKDQSEQETSADQHVTSNASDSE----- 712

Query: 744 XXXXXXXXXXXXXVLSYEAQRLSINYTRPVIIILGPLKDRINDDLISEYDPKFGSCVPHTT 803
VLSYE V + +NYTRPVIIILGP+KDRINDDLISE+PKFGSCVPHTT
Sbjct: 713 ---SSYRGQEYVLSYEPVNVQEVNYTRPVIIILGPMKDRINDDLISEFPDKFGSCVPHTT 769

Query: 804 RPKREYEVDRDYHFVSSREQMERDIQNHLEAGQYNDNLYGTSVASVREVAEKGHCI 863
RPKR+YEVDRDYHFV+SREQME+DIQ H FIEAGQYN++LYGTSV SVREVA KGKHCI
Sbjct: 770 RPKRDYEVDRDYHFVTSREQMEKDIQEHKFIAGQYNNHLYGTSVQSVREVAGKHCI 829

Query: 864 LDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRMTEEQAKKTYERAIKMEQEFGEY 923
LDVSGNAIKRLQ+AQLYP+++FIKPKS++++MEMN+R+TEEQA+KT+ERA+K+EQEF E+
Sbjct: 830 LDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNKRLTEEQARKTFERAMKLEQEFTEH 889

Query: 924 FTGVVQGDTEIEIYSKVKSMIWSQSGPTIWPVSKESL 960
FT +VQGDTE+IY++VK +I QSG IWVP+KE L
Sbjct: 890 FTAIVQGDTELDIYNQVKQIEEQSGSYIWPVPAKEKL 926

Score = 206 bits (524), Expect = 2e-51
Identities = 119/227 (52%), Positives = 146/227 (63%), Gaps = 30/227 (13%)

(SEQ ID NO:281)

(SEQ ID NO:282)

(SEQ ID NO:283)

(SEQ ID NO:284)

Query: 24 LFNLDSE-----VNGDDSEWLYEDIQLERGNGLGFSIAGGTDNPHIGTDTSIYITKLIS 76
L N DS VNG D+ + YE+I LERGNGLGFSIAGGTDNPHIG D+SI+ITK+I+
Sbjct: 201 LVNTDSLETPTYVNGTDADYEYEBITLERGNGLGFSIAGGTDNPHIGDDSSIFITKIIT 260

Query: 77 GGAAAADGRLXXXXXXXXXXXXXXXXXPHASAVDALKKAGNVVVLHVKKRXXXXXXXXXXXX 136
GGAAA DGRL H+ AV+ALK+AG++V+L+VKR+
Sbjct: 261 GGAAAQDGRLRVNDCILQVNEVDVRDVTHTSKAVEALKEAGSIVRLYVKKRKPVSSE----- 315

Query: 137 XXXXXXXXXXXXXXXXKVEIDLKVGKGLGFSIAGGIGNQHIPGNGIYVTKLTDGGRAQV 196

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K++EI L+KG KGLGFSIAGG+GNQHIPGDN IYVTK+ +GG A
Sbjct: 316 -----KIMEIKLIKPKGLGFSIAGGVGNQHIPGDN SIYVTKIIEGGAHK 361

Query: 197 DGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIGK 243
DG+L IGDKL+AV + LE VTHE AV LK+ +D V L + K
Sbjct: 362 DGKLQIGDKLLAV---NNVCLEEVTHEEAVTALKNTSDFVYLKVAK 404
Score = 88.2 bits (217), Expect = 7e-16
Identities = 68/234 (29%), Positives = 95/234 (40%), Gaps = 43/234 (18%)



Query: 40 DIQLERGNISGLGFSIAGGTDPHIGTDTSIYITKLISGAAAADGRLXXXXXXXXXXXXX 99
+I+L +G GLGFSIAGG N HI D SIY+TK+I GGAA DG+L
Sbjct: 319 EIKLIKGPGLGFSIAGGVGNQHIPGDN SIYVTKIIEGGAHKDGKLQIGDKLLAVNNVC 378

(SEQ ID NO:285)

(SEQ ID NO:286)

Query: 100 XXXXPHASAVDALKKAGNVVVLHVVRKXXXXXXXXXXXXXXXXXXXXXKVI----- 153
H AV ALK + V L V + V
Sbjct: 379 LEEVTHEEAVTALKNTSDFVYLKVAKPTSMYMNQGYAPPDITNSSSQPVDNHVSPSSFLG 438

Query: 154 -----EIDLKVGKGLGFSIAGGIGNQHIPGDN SIYVTKIIEGGAHKDGKLQIGDKLLAVNNVC 378
++ L +G GLGF+I GG + GI+++
Sbjct: 439 QTPASPARYSPVSKAVLGDDEITREPRKVVLRHGSTGLGFNIVGGEDGE-----GIFIS 492

Query: 187 KLTGGRQAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLI 240
+ GG A + G L GD++I+V + +L +HE A A LK+ VT++
Sbjct: 493 FILAGGPADLGSGLRKGDRISV---NSVDLRAASHEQAAAALKNAGQAVTIV 542
Score = 70.1 bits (170), Expect = 2e-10
Identities = 47/141 (33%), Positives = 69/141 (48%), Gaps = 12/141 (8%)



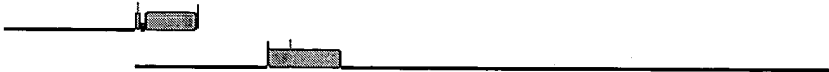
Query: 432 MPALPVESNQTNNSQSPQPRQPGSRVASTNVLAAPPGTTPRAVSTEDITREPRITITIQK 491
+P LPV + T PQ P +T+ L TP V+ D E IT+++
Sbjct: 176 IPVLPVPAENTVILPTIPQANPPPV-LVNTDSLE-----TPTYVNGTDADYEYEEITLER 229

(SEQ ID NO:287)

(SEQ ID NO:288)

Query: 492 GPQGLGFNIVGGEDG-----QGIYVSFILAGGPADLGSSELKRGDQLLSVNNVNLTHATH 545
G GLGF+I GG D I+++ I+ GG A L+ D +L VN V++ TH
Sbjct: 230 GNSGLGFSIAGGTDPHIGDDSSIFITKIITGAAAQDGRRLRVNDCILQVNEVDVRDVTH 289

Query: 546 EEAAQALKTSGGVVTLAQYR 566
+A +ALK +G +V L + R
Sbjct: 290 SKAVEALKEAGSIVRLYVKRR 310
Score = 67.4 bits (163), Expect = 1e-09
Identities = 39/81 (48%), Positives = 49/81 (60%), Gaps = 6/81 (7%)



Query: 487 ITIQKGPQGLGFNIVGGEDGQ-----GIYVSFILAGGPADLGSSELKRGDQLLSVNNVNL 540
I + KGP+GLGF+I GG Q IYV+ I+ GG A +L+ GD+LL+VNNV L
Sbjct: 320 IKLIKGPGLGFSIAGGVGNQHIPGDN SIYVTKIIEGGAHKDGKLQIGDKLLAVNNVCL 379

(SEQ ID NO:289)

(SEQ ID NO:290)

Query: 541 THATHEEAQALKTSGGVVTL 561
THEEA ALK + V L
Sbjct: 380 EEVTHEEAVTALKNTSDFVYL 400

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FIGURE 6B

CLUSTAL W (1.82) sequence alignment

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Drosophila  MTTRKKKRDGGGSGGGFIKKVSSLFNLDSVNGDDSWLYEDIQLERGNLGLFSIAGGTDN 60
Human       MPVRKQD-----TQRALHLLLEEYRSKLSQTEDRQLRSSIERVINIFQSNLFQ 47
          *..**:.          .. :.* .   .   ** ** . . . : . . . :

Drosophila  PHIGTDTSIYITKLISGGAAAADGRLSINDIIVSVNDVSVVDVPHASAVDALKKAGNVVK 120
Human       ALIDIQEFYEVTLTDN--PKCID-RSKPSEPIQPVNTWEISSLPSTVTSETLPSSLSPS 104
          . * . :   : * * . . . * . . : * ** . : . : * : . . . : . .

Drosophila  LHVKRKRGTATTAAAGSAAGDARDAASAGPKVIEIDLKGGKGLGFSIAGGIGNQHIPGD 180
Human       VEKYRYQDEDTTPQEHISP--QITNEVIGPELVHVSEKN--LSEIENVHGFVSHSHIS-P 159
          :. * :.  *. *   :.   . . **:::.. :   .   . : * :. :. **.

Drosophila  NGIYVTKLTGGRAQVDGRLSIGDKLIAVRTNGSEKN---LENVTHELAVATLKSITDKV 237
Human       IKPTEAVLPSPTVPVPIVLPVPAENTVILPTIPQANPPVPLVNTDSLETPTYVNGTDAD 219
          : *.. . . *   * . : : . : . . : *   :   *..* . . * . **

Drosophila  TLIIGKTQHLTTSAS---GGGGGGLSSGQQLSQSQSLATSQSQSQVHQQQHATPMVNS 293
Human       YEYEEITLERGNLGLFSIAGGTDNPHIGDDSSIFITKIITGGAAQDGRLRVNDCILQV 279
          * . . *.   . ** ..   * : : *   : : : * . : : *   : :   : :

Drosophila  QSTGALNSMGQTVDSPSIPQAAAAVAAAANASASASVIASNNNTISNTTVTTVTATATAS 353
Human       NEVDVRDVTHTSKAVEALKEAGSIVRLYVKKRKPVSEKIMEIK-LIKGPKGLGFSIAGGVG 338
          : . . . :   . . * : : . . : . . . . . * . : :   : * . . .   . : . .

Drosophila  NDSSKLPPSLGANSSISISNSNSNSNSNNINNINSINNNSSSSSTTATVAAATPTAASA 413
Human       NQHIPGDNISYVTKIIEGGAHKGDKLQIGDKLLAVNNVCLEEVTHEEAVTALKNTSDFV 398
          * :   * : . . * . . : : : : : : : : : : : : : : : : : : : : :

Drosophila  AAAAASSPPANSFYNNASMPALPVESNQTNRSQSPQPRQPGSRYASTNVLAAPPGTTPR 473
Human       YLKVAK-PTSMYMNDGYAPPDITNSSSQPVDNHVSPSS-FLGQTPASP--ARYSPVSKA 453
          . * . * . : : : : * : . . * . . .   . . .   . * .   . * .   . * :

Drosophila  AVSTEDITREPRITITQKGPQGLGFNIVGGEDGQGIYVSFILAGGPADLGSSELKRGDQLL 533
Human       VLGDEITREPRKVVLRHGSTGLGFNIVGGEDGEGIFISFILAGGPADLGSSELKRGDRII 513
          : . . : : * * * * . : : : * . * * * * * * * * * * * * * * * * * * : : : : :

Drosophila  SVNNVNLTHATHEEAAQALKTSGGVVTLAQYRPEEYNRFEARIQELKQQAALGAGGSGT 593
Human       SVNSVDLRAASHEQAAAALKNAGQAVTIVAQYRPEEYSRFEAKIHDLEQMMNSSISSGS 573
          *** . * : * : * : * * * . * . * : : * * * * * * * * * * * : : * : : . : * :

Drosophila  -LLRTTQKRSLYVRALFDYDPNRDDGLPSRGLPFKHGDILHVTNASDDEWWQARRVLGDN 652
Human       GSLRTSQKRSLYVRALFDYDKTKDGLPSQGLNFKFGDILHVINASDDEWWQARQVTPDG 633
          *** : * * * * * * * * * * . : * . * * * : * * . * * * * * * * * * * : * .

Drosophila  EDEQIGIVPSKRRWERKMRARDSVKFQGHAAANNLKDQSTLDRKKKNFTFSRKFPFMK 712
Human       ESDEVGVI PSKRRVEKKERARLKTVKFN-----SKTRDKGQSFNDKRRKNLFSRKFPFYK 688
          * . : : : : * * * * * * * * * * : * * :   . . * * . : : * : * :   * * * * * *

Drosophila  SRDEKNEDGSDQEPNGVVSSTSEIDINNVMNNQSNQEPQSEENVLSYEAVQRLSINYTRP 772
Human       NKDQSEQETSDADQH-VTSNASDSESSYRGQ-----EEVLSYEPVNQEQEVNYTRP 738
          . : * : : : * * : : * . * : * : . .   .   .   .   .   .   .   .   .   .   .   .

Drosophila  VIILGPLKDRINDDLISEYDPKFGSCVPHTTRPKREYVDGRDYHFVSSREQMERDIQN 832
Human       VIILGPMKDRINDDLISEFPDKFGSCVPHTTRPKRDYVDGRDYHFVTSREQMEKDIQEH 798
          * * * * * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  
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(SEQ ID NO:291)
(SEQ ID NO:267)

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Drosophila	LFIEAGQYNDNLYGTSVASVREVAEKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVD 892
Human	KFIEAGQYNNHLYGTSVQSVREVAGKGKHCILDVSGNAIKRLQIAQLYPISIFIKPKSME 858
	*****;:***** ***** *****;*****;:*****;:
Drosophila	SVMEMNRRMTTEEQAKKTYERAIKMEQEFGEYFTGVVQGDTEEEIYSKVKSMIWSQSGPTI 952
Human	NIMEMNKRLEEQARKTFERAMKLEQEFTEHFTAIVQGDLEDIYNQVKQIIIEQSGSYI 918
	.:****;*:*****;*:***;*:***** *:***:*****;*:***:***.* ****.*
Drosophila	WVPSKESL 960
Human	WVPAKEKL 926
	:.*


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FIGURE 6C

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 2

BLASTP sequence alignment

Score = 621 bits (1601), Expect = e-176
Identities = 318/524 (60%), Positives = 390/524 (73%), Gaps = 43/524 (8%)



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Query: 438 ESNQTNNRSQSPQPRQPGSRYSTNVLAAPPPTPRAVSTEDITREPTITIQKGPQGLG 497
      +S T++ S RQP RAVS E EPR + + KG GLG
Sbjct: 389 DSEMTSHSQHSTATRQPSMTLQ-----RAVSLEG---EPRKVV LHKGSTGLG 432

Query: 498 FNIVGGEDGQGIYVSFILAGGPADLGSSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGG 557
      FNIVGGEDG+GI+VSFILAGGPADL EL+RGDQ+LSVN ++L A+HE+AA ALK +G
Sbjct: 433 FNIVGGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDLRGASHEQAAAALKGAGQ 492

Query: 558 VVTLAQYRPEEYNRFEARIQELKQXXXXXXXXXXXXXXXXX-QKRSLYVRALFDYDPNRD 616
      VT++AQY+PE+Y RFEA+I +L++Q QKRSLYVRA+FDYD ++D
Sbjct: 493 TVTIIAQYQPEDYARFEAKIHDLREQMMNHSMSGSGSLRTNQKRSLYVRAMFDYDKSKD 552

Query: 617 DGLPSRGLPFKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVPSKRRWERKMRARDRS 676
      GLPS+GL FK+GDILHV NASDDEWWQARRV+ + + E++G++PSKRR ERK RAR ++
Sbjct: 553 SGLPSQGLSFKYGDILHVINASDDEWWQARRVMLEGDSEEMGVIPSKRRVERKERARLKT 612

Query: 677 VKFQGHAAANNLNDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEGSDQEPNGVVSSTSEI 736
      VKF ++ K S D++KK+F FSRKFPF K++++ ++ SD E +
Sbjct: 613 VKFNAKPGVIDS--KGSFNDKRKKSFIKSRKFPFYKNEQSEQETS DPE-----RGQE 663

Query: 737 DIXXXXXXXXXXXXXXXXXXVLSYEAVQRLSINYTRPVIILGPLKDRINDDLISEYDPKFG 796
      D+ +LSYE V R INYTRPVIILGP+KDRINDDLISE+PDKFG
Sbjct: 664 DL-----ILSYEPVTRQEINYTRPVIILGPMKDRINDDLISEFPDKFG 706


Query: 797 SCVPHTTRPKREYVDGRDYHFVSSREQMERDIQNHLFIEAGQYNDNLYGTSVASVREVA 856
      SCVPHTTRPKR+YEVDGRDYHFV SREQME+DIQ H FIEAGQYNDNLYGTSV SVR VA
Sbjct: 707 SCVPHTTRPKRDYEVVDGRDYHFVISREQMEKDIQEHKFIEAGQYNDNLYGTSVQSVRFVA 766

Query: 857 EKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRMTEEQAKKTYERA IKM 916
      E+GKHCILDVSGNAIKRLQVAQLYP+A+FIKP+S++S+MEMN+R+TEEQAKKTY+RAIK+
Sbjct: 767 ERGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLSLMEMNKRLEEQAKKTYDRAIKL 826

Query: 917 EQEFGYFTGVVQGDITIEEYISKVKSMIWSQSGPTIWVPSKESL 960
      EQEFGYFT +VQGD+T+E+IY++ K +I QSGP IW+PSKE L
Sbjct: 827 EQEFGYFTAIVQGDITLEDIYNQCKLVIEEQSGPFIWIPSKESL 870
Score = 197 bits (502), Expect = 7e-49
Identities = 111/221 (50%), Positives = 140/221 (63%), Gaps = 24/221 (10%)
  
```

(SEQ ID NO:259)

(SEQ ID NO:292)



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Query: 23 SLFNLDVSGDD-SWLYEDIQLERGNGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAA 81
      +L + VNG + + +E+I LERGNGLGFSIAGGTDNPHIG D I+ITK+I GGAAA
Sbjct: 80 TLDTIPYVNGTEIEYEFEEITLERGNGLGFSIAGGTDNPHIGDDPGIFITKIIPGGAAA 139

Query: 82 ADGRLXXXXXXXXXXXXXXXXXPHASAVDALKKAGNVVVLHVVRKXXXXXXXXXXXXXXXXX 141
      DGRL H+ AV+ALK+AG++ +L+V+R+
Sbjct: 140 EDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARLYVRRRRPILET----- 190
  
```

(SEQ ID NO:293)

(SEQ ID NO:294)

MARKED-UP VERSION

12/19

Query: 142 XXXXXXXXXXKVEIDLKVGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLS 201
V+EI L KG KGLGFSIAGG+GNQHIPGDN IYVTK+ DGG AQ DGRL
Sbjct: 191 -----VVEIKLFKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRQLQ 240

Query: 202 IGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIG 242
+GD+L+ V + +LE VTHE AVA LK+ ++ V L +G
Sbjct: 241 VGDRLLMV----NNYSLEEVTHEEAVAILKNTSEVVYLKVG 277
Score = 66.2 bits (160), Expect = 3e-09
Identities = 40/125 (32%), Positives = 64/125 (51%), Gaps = 11/125 (8%)



Query: 448 SPQPRQPGSRYASTNVLAAPPGTPRAVSTEDITREPTITIQKGPQGLGFNIVGGEDGQ 507
SP P +T+ L +P V+ +I E IT+++G GLGF+I GG D
Sbjct: 65 SPLKASPAPIIVNTDLDLTIP-----YVNGTEIEYEFEEITLERGNSGLGFSIAGGTDNP 119

Query: 508 -----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTL 561
GI+++ I+ GG A L+ D +L VN V+++ +H +A +ALK +G + L
Sbjct: 120 HIGDDPGIFITKIIPGAAAEDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARL 179

Query: 562 LAQYR 566
+ R
Sbjct: 180 YVRRR 184
Score = 65.5 bits (158), Expect = 5e-09
Identities = 38/81 (46%), Positives = 47/81 (57%), Gaps = 6/81 (7%)



Query: 487 ITIQKGPQGLGFNIVGGEDGQ-----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNL 540
I + KGP+GLGF+I GG Q IYV+ I+ GG A L+ GD+LL VNN +L
Sbjct: 194 IKLFKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRQLQVGDRLLMVNNYSL 253

Query: 541 THATHEEAAQALKTSGGVVTL 561
THEEA LK + VV L
Sbjct: 254 EEVTHEEAVAILKNTSEVVYL 274
Score = 50.8 bits (120), Expect = 1e-04
Identities = 33/87 (37%), Positives = 48/87 (54%), Gaps = 10/87 (11%)



Query: 154 EIDLKVGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNG 213
++ L KG GLGF+I GG + GI+V+ + GG A + G L GD+++V NG
Sbjct: 421 KVVHLKGSTGLGFNIVGGEDGE-----GIFVSFILAGGPADLSGELQRGDQILSV--NG 472

Query: 214 SEKNLENVTHELAVATLKSITDKVTLI 240
+ L +HE A A LK VT+I
Sbjct: 473 ID--LRGASHEQAAAALKGAGQTVTII 497
Score = 41.2 bits (95), Expect = 0.10
Identities = 24/81 (29%), Positives = 36/81 (43%), Gaps = 6/81 (7%)



Query: 41 IQLERGNISGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLXXXXXXXXXXXXX 100
+ L +G+++GLGF+I GG D I+++ +++GG A G L
Sbjct: 422 VVLHKGSTGLGFNIVGGEDG-----EGIFVSFILAGGPADLSGELQRGDQILSVNGIDL 475

Query: 101 XXXPHASAVDALKKAGNVVKL 121
H A ALK AG V +
Sbjct: 476 RGASHEQAAAALKGAGQTVTI 496

(SEQ ID NO:295)

(SEQ ID NO:296)

(SEQ ID NO:297)

(SEQ ID NO:298)

(SEQ ID NO:299)

(SEQ ID NO:300)

(SEQ ID NO:301)

(SEQ ID NO:302)

FIGURE 6D

CLUSTAL W (1.82) sequence alignment

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Drosophila -----MTTRKKKRDGG----- 11
Human MFFACYCALRTNVKKYRYQDEDA PHDHS L PRLTHEVRGP ELVHVSEKNLSQIENVHGYVL 60
      * . * * .

Drosophila -----GSGGGFIKKVSSLFNLDVNG-DDSWLYEDIQLERGN SGLGFSIAGGTDNPH 62
Human QSHISPLKASPAPIIVNTDTLDTIPYVNGTEIEYEFEEITLERGN SGLGFSIAGGTDNPH 120
      . * . : * : . : * : * * : . : : * * * * * * * * * * * * * * * *

Drosophila IGTDTSIYITKLISGGA AADGR LSINDIIVSVNDVSVVDVPHASAVDALKKAGNVVKLH 122
Human IGDDPGIFITKIIIPGGA AEDGR LRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARLY 180
      * * . . : * * : * . * * * * : * * : * * : * * : * . : . : * * : * :

Drosophila VKRKRGTATTPAAGSAAGDARDSAASGPKVIEIDLKGGKGLGFSIAGGIGNQH I PGDNG 182
Human VRRRRPILET-----VVEIKLFKGP KGLGFSIAGGVGNQH I PGDNS 221
      * : * : * * * * * * * * * * * * * * * * * * * * * * * * * * * *

Drosophila IYVTKLTDGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIG 242
Human IYVTKIIDGGAAQKDGR LQVGDRLLMVNN---YSLEEVTHEEAVAILKNTSEVVYLKVG 277
      * * * * : * * * * * * * * * * : * * : * . . . * * : * * * * * * * * *

Drosophila KTQHLTTSASGGGGG LSSGQQLS QSQSLATSQS QSQVHQQHATPMVNSQSTGALNSM 302
Human NPTTIYMTDPYGP-----PDITHS-----YSPPMEN----- 303
      : . : : * : : : * : : : * * * *

Drosophila GQTVVDSPSP IQAAA AAAAAA SASASV IASNN TISNTT VTTV TATATASNDSSKLPPS 362
Human -----HLLSGNN-----GTLEYKTS LPPIS 323
      : : : * * * * * * * * * * * * * * * * * * * * * * * * * * *

Drosophila LGANSSISISNSNSNSNNINNINSINNNSSSSSTTATVAAATPTAASAAAAA ASSPP 422
Human PGRYSPIPKHMLVDDDYTRPPEPVYSTVNKLCDKP-----ASPRHYPVECDKSFL 375
      * * * . : . : : : * * : . . . * : * * . . *

Drosophila ANSFYNNASMPALPVESNQTNNSRSQSPQRPQGSRYASTNVLA AVPPGTPRAVSTEDITR 482
Human S-APYSHYHLGLLP-DSEMTSHSQHSTATRQP-----SMTLQRAVSLE---G 417
      : : * : : * * : * : : * . * * * * * * * * * * * * * * *

Drosophila EPRTITIQKPGQGLGFNI VGGEDGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTH 542
Human EPRKVV LHKGSTGLGFNI VGGEDGEGIFVSFILAGGPADL SGE LQRGDQILSVNGIDLRG 477
      * * . : : * * * * * * * * * * : * * : * * * * * * * * * * * * * * *

Drosophila ATHEEAQA LKTSGGVV TLLAQYRPEEYNRFEARIQELKQQAALGAGGSGT-LLRTTQKR 601
Human ASHEQAAAALKGAGQTVTIIAQYQPEDYARFEAKI HDLREQMMNHSMSGSGSLRTNQKR 537
      * : * : * * * * * * : * * : * * : * * * * * : * * : * * : * * * *

Drosophila SLYVRALFDYDPNRDDGLPSRGLPFKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVP 661
Human SLYVRAMFDYDKSKDGLPSQGLSF KYGDILHVINASDDEWWQARRVMLEGDSEEMGVIP 597
      * * * * : * * * * * : * * : * * * * * * * * * * * * * * : . : * : : * *

Drosophila SKRRWERKMRARDSVKFQGHAAANNNDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDG 721
Human SKRRVERKERARLKT VKNAPKPGVID--SKGSFNDKRKKS FIFSRKFPFYKNKEQSEQET 655
      * * * * * * * * : * * : . : . : : * * * * : * * * * * * * * : : : : :

Drosophila SDQEPNGVVSSTSEIDINN VNNQSN EPQ PSEENVLSYEAVQRLSIN YTRPVIILGPLKD 781
Human SDPE-----RGQEDLILSYEPVTRQEIN YTRPVIILGPMKD 691
      * * * : . : : * * * * * * * * * * * * * * * * * * * * * * * *

Drosophila RINDDLISEY PDKFGSCVPHTTRPKREYEVDGRDYHFVSSREQMERDIQNH LFI EAGQYN 841
Human RINDDLISEY PDKFGSCVPHTTRPKRDYEVDGRDYHFVISREQMEKDIQEHKFIEAGQYN 751
      * * * * * * * * : * * : * * * * * * * * * * * * * * * * * * * * * *

Drosophila DNLYGTSVASVREVAEKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRM 901
Human DNLYGTSVQSVRFVAERGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLES LMEMNKRL 811
      * * * * * * * * : * * : * * * * * * * * * * : * * * * : * * : * * : *

Drosophila TEEQAKKTYERAIKMEQEFGEYFTGVVQGD TIEE IYSKVKS MIWSQSGPTIWVPSKESL 960
Human TEEQAKKTYDRAIKLEQEFGEYFTAIVQGD TLEDIYNQCKLVIEEQSGPFIWIWPSKEKL 870
      * * * * * * * * : * * : * * * * * * : * * : * * * * * * * * * * *

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(SEQ ID NO:261)
(SEQ ID NO:303)

FIGURE 7

Hu-Dlg1	---MPVRKQDTQRALHLLLEEYRSKLSQTEDRQLRSSIERVINIFQSNLFQ-ALIDIQEFY	56
Hu-Dlg4	---MSQRPRAPRSALWLLAPLLRWAPP-----LLTVLHSDLFQ-ALLDILDY	45
Hu-Dlg2	---MFFACYCALRTNVKKYRYQDEDA PHDS-----LPRLTHEVRGP-ELVHVSEK-	47
Hu-Dlg3	MHKHQHCKCCECYEVTRLAALRRLEPPGYG----DWQVPDPYGPGGNGASAGYGGYS	55
Dm-Dlg1	---MTTRKK-----KRDGG-----	11
Hu-Dlg5	-----	
Hu-Dlg1	EVTLLDNPKCIDRSKPSEPIQPVNTWEISSLPSSVTSETLPSSLSPSVEKYRYQDEDT	116
Hu-Dlg4	EASLSES-----QKYRYQDEDT	63
Hu-Dlg2	NLSQIEN-----VHGYVLQSHISP	66
Hu-Dlg3	SQTLPSQAG-----ATPTPRTKAKLIP	77
Dm-Dlg1	-----	
Hu-Dlg5	-----	
Hu-Dlg1	PQEHISPQITNEVIGPELVHVSEKNLSEIENVHGFVSHSHISPIKPTEAVLPSPPTVPVI	176
Hu-Dlg4	PLEHSP-----AHLPN-----	74
Hu-Dlg2	LK-----	68
Hu-Dlg3	TGRDVG-----PVPLKPVPGK-----	93
Dm-Dlg1	-----	
Hu-Dlg5	-----	
Hu-Dlg1	PVLVPVAENTVILPTIPQANPPVVLVNTDSLETP---TYVNGTDADYEEIEITLERGNSG	233
Hu-Dlg4	-----QANSPPVIVNTDTLEAPGYELQVNGTEGEMEYEEITLERGNSG	117
Hu-Dlg2	-----ASPAPIIVNTDTLDTIP---YVNGTEIEYEFEEITLERGNSG	107
Hu-Dlg3	-----STPKLNGSGSPWWPECTCTNRDWYEQVNGSDGMFKYEEIVLERGNSG	140
Dm-Dlg1	-----GSGGGFIKKVSSLFNLD---SVNGDD-SWLYEDIQLERGNSG	49
Hu-Dlg5	-----MRATHGSNSLPSSARLGSSSN	21
*.*	
Hu-Dlg1	LGFSIAGGTDNPHIGDDSSIFITKII TGGAAAQDGRRLVNDCILQVNEVDVRDVTHSKAV	293
Hu-Dlg4	LGFSIAGGTDNPHIGDDPSIFITKII PGGAAAQDGRRLVND SILVNEVDVREVTHSAAV	177
Hu-Dlg2	LGFSIAGGTDNPHIGDDPGIFITKII PGGAAAEDGRLRVND CILRVNEVDVSEVSHSKAV	167
Hu-Dlg3	LGFSIAGGIDNPHVPDDPGIFITKII PGGAAAMDGR LGVND CVLRVNEVEVSEVHSHRAV	200
Dm-Dlg1	LGFSIAGGTDNPHIGTDTSIYITKLI SGGAAAADGR LSI ND I IVSVNDVSVVDVPHASAV	109
Hu-Dlg5	LQFKAER- IKIPSTPRYPRSVVGSER--GSVSHSECSTPPQSPLNIDTLSSCSQSQTAS	78
	* * . * . : . * : . : : : . : : *	
Hu-Dlg1	EALKEAGSIVRLYVKRRK-----PVS-----EKIMEIKLIKGP KGLGFSI	333
Hu-Dlg4	EALKEAGSIVRLYVMRRK-----PPA-----EKVMEIKLIKGP KGLGFSI	217
Hu-Dlg2	EALKEAGSIARLYVRRRR-----PIL-----ETVVEIKLFKGP KGLGFSI	207
Hu-Dlg3	EALKEAGPVVRLVRRRQ-----PPP-----ETIMEVNLLKGP KGLGFSI	240
Dm-Dlg1	DALKAGNVVVLHVKKRR-GTATTPAAGSAAGDARD SAASGPKVIEIDL VKGGKGLGFSI	168
Hu-Dlg5	TLPRIAVNPASLGERRKDR---PYV-----EEPRHVKVQKGSEPLGISI	119
	: * . * * : . . : : : * : * : * : *	
Hu-Dlg1	AGGVGNQH IPGDNSIYVTKI IEGGAAHKDGKLQIGDKLLAVNN---VCLEEVTHEEAVT	389
Hu-Dlg4	AGGVGNQH IPGDNSIYVTKI IEGGAAHKDGRLQIGDKILAVNS---VGLEDVMHEDAVA	273
Hu-Dlg2	AGGVGNQH IPGDNSIYVTKI IDGGAAQKDGR LQVGDRLLMVNN---YSL EEVTHEEAVA	263
Hu-Dlg3	AGGIGNQH IPGDNSIYITKI IEGGAAQKDGR LQIGDRLLAVNN---TNLQDVRHEEAVA	296
Dm-Dlg1	AGGIGNQH IPGDNGIYVTKLTDGGR AQVDGR LSI GDKLIAVRTNGSEKNLENVTHELAVA	228
Hu-Dlg5	VSGE-----KGGIYVSKVTVGSIAHQAG-LEYGDQLLEFNG---INLRSATEQQARL	167
	..* . . . * : * . * : * * . * : : . . * . . : *	
Hu-Dlg1	ALKNTSDFVYLK VAKPTSMYMN DGYA-----	415
Hu-Dlg4	ALKNTYDVVYLK VAKPSNAYLS DSYA-----	299
Hu-Dlg2	ILKNTSEVVYLK VGNPTTIYMDPYG-----	289
Hu-Dlg3	SLKNTSDMVYLK VAKPGSLHLNDMYA-----	322
Dm-Dlg1	TLKSITDKVTLI IGKTQH LTT SASGGGGGLSSGQQLSQS QSLATSQS QSVHQQQHAT	288
Hu-Dlg5	IIGQQCDTITILAQYNPHVHQLSSH-----	193
	: . : : :	
Hu-Dlg1	-----	
Hu-Dlg4	-----	
Hu-Dlg2	-----	
Hu-Dlg3	-----	
Dm-Dlg1	PMVNSQSTGALNSMGQTVVDSPSIPQAAAAVAAAANASASASV IASNNTISNTTVTTVTA	348

(SEQ ID NO:267)
(SEQ ID NO:304)
(SEQ ID NO:303)
(SEQ ID NO:305)
(SEQ ID NO:259)
(SEQ ID NO:306)

MARKED-UP VERSION

15/19

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Hu-Dlg5 -----

Hu-Dlg1 -----PP-----DITNSSSQVDNHVS-----PSSFLG----- 438
Hu-Dlg4 -----PP-----DITTSYSQHLNEIS-----HSSYLGTD-----YP 326
Hu-Dlg2 -----PP-----DITHSYSPPMENHLL-----SGNNGTLE-----YK 316
Hu-Dlg3 -----PP-----DYASTFTALADNHIS-----HNSSLGYLGAVESKVS 356
Dm-Dlg1 TATASNDSSKLPPSLGANSSISISNSNSNSNNINNINSINNNSSSSSSTTATVAAATP 408
Hu-Dlg5 -----RSSSHLDPAAGTHSTLQ-----GSGTTTPEHPSVIDPLM 226
      . : : . . .

Hu-Dlg1 --QTPASPARYSPPVSKAVLGDDEITR----- 462
Hu-Dlg4 TAMTPTSPRRYSPVAKDLLGEEDI PR----- 352
Hu-Dlg2 TSLPPISPGRYSPIPKHMLVDDDDYTRPPEPVYSTVNKLCDKPASPRHYSPECDKSFLLS 376
Hu-Dlg3 PAPPQVPPTRYSPIPRHMLAEEDFTR----- 382
Dm-Dlg1 TAASAAAAAASSPPANSFYNNASMPALPVESNQTNNRSQSPQPRQPGSRYASTN----- 462
Hu-Dlg5 EQDEGPSTPPAKQSSSRIAGDANKKT----- 252
      . . . . . : .

Hu-Dlg1 -----EPRKVVLHRGSTGLGFNIV 481
Hu-Dlg4 -----EPRRIVIHRRGSTGLGFNIV 371
Hu-Dlg2 APYSHYHLGLLPDSEMTSHSQHSTATRQPSMTLQRAVSLEGEPRKVVLHKGSTGLGFNIV 436
Hu-Dlg3 -----EPRKIILHKGSTGLGFNIV 401
Dm-Dlg1 -----VLAAVPPGT PRAVSTEDITREPTITIQKGPQGLGFNIV 501
Hu-Dlg5 -----LEPRVVFIIKKSQLELGVHLC 272
      *** : : : . ** : :

Hu-Dlg1 GGEDGEGIFISFILAGGPADLSGELRKGDRIISVNSVDLRAASHEQAAAAALKNAGQAVTI 541
Hu-Dlg4 GGEDGEGIFISFILAGGPADLSGELRKGDQILSVNGVDLRNASHEQAAIALKNAGQTVTI 431
Hu-Dlg2 GGEDGEGIFVSFILAGGPADLSGELRQGDQILSVNGIDLRGASHEQAAAAALKGAGQTVTI 496
Hu-Dlg3 GGEDGEGIFVSFILAGGPADLSGELRRGDRILSVNGVNLNRNATHEQAAAAALKRAGQSVTI 461
Dm-Dlg1 GGEDGQGIYVSFILAGGPADLSGELRKGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTL 561
Hu-Dlg5 GG-NLHGVPVAEVEDDSPAKGPDGLVPGLDILEYGLDVRNKTVEEVYVEMLKPRDGVRL 331
** : . * : : : : . . * . * * : : . : : : : * : . : . * :

Hu-Dlg1 VAQYRPEEYSRFEAKIHDLEQMMNSSISSGSGSLRTSQKRSLYVRALFDYDKTKDSGLP 601
Hu-Dlg4 IAQYKPEEYSRFEAKIHDLEQMLNSSLGSGTASLRSNPKRGFYIRALFDYDKTKDCGFL 491
Hu-Dlg2 IAQYQPEDYARFEAKIHDLEQMMNHSMSGSGSLRTNQKRSLYVRAMFDYDKSKDSGLP 556
Hu-Dlg3 VAQYRPEEYSRFEAKIHDLEQMMNSSMSGSGSLRTSEKRSLYVRALFDYDRTRDSCLP 521
Dm-Dlg1 LAQYRPEEYNRFEARIQELKQQAALGAGGSGT-LLRTTQKRSLYVRALFDYDPNRDDGLP 620
Hu-Dlg5 KVQYRPEEFTKAG-----LPGDSFYIRALYDR-----LADV 363
      . * : * : : : : . . . . . : * : * : * :

Hu-Dlg1 SQGLNFKFGDILHVINASDD---EWWQARQVTPDGESDEVGVI PSKRRVEKKERARLKT 658
Hu-Dlg4 SQALSFRFGDVLHVIDASDE---EWWQARRVHSDSETDDIGFIPSKRRVERREWSRLKAK 548
Hu-Dlg2 SQGLSFKYGDILHVINASDD---EWWQARRVMLEGDSEEMGVIPSKRRVERKERARLKT 613
Hu-Dlg3 SQGLSFSYGDILHVINASDD---EWWQARLVTPHGESEQIGVIPSKRRVEKKERARLKT 578
Dm-Dlg1 SRGLPFFKHGDILHVTNASDD---EWWQARRVLGDNEDEQIGVIPSKRRWERKMRARDRSV 677
Hu-Dlg5 EQELSFKKDDILYVDDTLPGTFGSWMWQLDENAQKIQRGQIPSKYVMDQEFRRRLSMS 423
.: * * . * : * : : : * * : . : : * : * * : : . *

Hu-Dlg1 KFNSKT----RDKGQSFNDKRKKNLFSRKFPFYKNKDQSEQETSDADQH----- 703
Hu-Dlg4 DWG----- 551
Hu-Dlg2 KFNAKPGVI--DSKGSFNDKRKKSFI FSRKFPFYKNKEQSEQE----- 654
Hu-Dlg3 KFHARTGMI--ESNRDFPGLSDDYY----- 601
Dm-Dlg1 KFQGHAAANNLDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDGSDQEPNGVVSSTSEID 737
Hu-Dlg5 EVKDDNSATKTL SAAARRSFFRRKHKHKRSGSKDGKDLLALDAFS----- 468
      .

Hu-Dlg1 VTSNASDSESSYRGQEEYVLSYEPVNQQEVNYTRPVII LGPMKDRINDDLISEFPDKFGS 763
Hu-Dlg4 -----SSSGSQGREDSVLSYETVTQMEVHYARP II LGPTKDRANDLLSEFPDKFGS 604
Hu-Dlg2 -----TSDPERGQEDLILSYEPVTRQEIYNYTRPVII LGPMKDRINDDLISEFPDKFGS 707
Hu-Dlg3 -----GAKNLKGQEDAILSYEPVTRQEIHYARPV II LGPMKDRVNDLISEFPDKFGS 654
Dm-Dlg1 INNVDNNQSNQEPQSEENVLSYEAQRLSINYTRPVII LGPLKDRINDDLISEYDPDKFGS 797
Hu-Dlg5 -----SDSIPLFEDSVSLAYQRVQKVDCTALRPVLI LGPLLDVVKEMLVNEAPGKFCR 521
      . : . * : * : . * : * : * : * : * : * : * : * : * :

Hu-Dlg1 CVPHTTRPKRDYEV DGRDYHFVTSREQMEKDIQEHKFI EAGQYNNHLYGTSVQSVREVAG 823
Hu-Dlg4 CVPHTTRPKREYIDGRDYHFVSSREKMEKDIQAHKFI EAGQYNSHLYGTSVQSVREVAE 664
Hu-Dlg2 CVPHTTRPKRDYEV DGRDYHFVTSREQMEKDIQEHKFI EAGQYNDNLYGTSVQSVRFAE 767
Hu-Dlg3 CVPHTTRPRRDNEVDGQDYHFVVSREQMEKDIQDNKFI EAGQFNDNLYGTSIQSVRAVAE 714
Dm-Dlg1 CVPHTTRPKREYEV DGRDYHFVSSREQMERDIQNHLEAGQYNDNLYGTSVASVREVAE 857
Hu-Dlg5 CPLEVMMK-----ASQQAIERGVKDCLFVDYKRRSGHFDVTTVASIXEITE 566
* . . : * : : * : : * : : * : : * : : * : : * : :

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